

1/16

## SEQUENCE LISTING

## 5 (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: ACTINOVA LIMITED  
(B) STREET: 5 Signet Court, Swanns Road  
10 (C) CITY: Cambridge  
(E) COUNTRY: United Kingdom  
(F) POSTAL CODE (ZIP): CB5 8LA

15 (ii) TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN

(iii) NUMBER OF SEQUENCES: 22

## 20 (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25 (v) CURRENT APPLICATION DATA:  
APPLICATION NUMBER: GB N/A

## (2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..246

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45 ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA  
Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu  
1 5 10 15

48

50 CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA  
Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly  
20 25 30

96

2/16

|    |  |     |
|----|--|-----|
|    | AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA<br>Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Ala Thr Ala     | 144 |
| 5  | 35                  40                  45   |     |
|    | GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT<br>Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr | 192 |
| 10 | 50                  55                  60   |     |
|    | ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT<br>Thr Ala Asp Leu Glu Asp Gly Asn His Met Asn Ile Lys Phe Ala     | 240 |
|    | 65                  70                  75                  80   |     |
| 15 | GGA AAA TAA<br>Gly Lys   | 249 |

## 20 (2) INFORMATION FOR SEQ ID NO: 2:

|    |   |  |
|----|---|--|
|    | (1) SEQUENCE CHARACTERISTICS:                                   |  |
|    | (A) LENGTH: 82 amino acids                                      |  |
| 25 | (B) TYPE: amino acid  |  |
|    | (C) TOPOLOGY: linear  |  |
|    | (D) MOLECULE TYPE: protein                                      |  |
|    | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:                        |  |
| 30 | Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu |  |
|    | 1                  5                  10                  15    |  |
|    | Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly |  |
| 35 | 20                  25                  30                      |  |
|    | Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Ala Thr Ala     |  |
|    | 35                  40                  45                      |  |
| 40 | Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr |  |
|    | 50                  55                  60                      |  |
|    | Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala |  |
|    | 65                  70                  75                  80  |  |
| 45 | Gly Lys   |  |

## (2) INFORMATION FOR SEQ ID NO: 3:

|    |                               |  |
|----|-------------------------------|--|
| 50 | (i) SEQUENCE CHARACTERISTICS: |  |
|    | (A) LENGTH: 228 base pairs    |  |
|    | (B) TYPE: nucleic acid        |  |

3/16

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5 (11) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION:1 22

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15 AAA GAA GAA ACA CCA GAA ACA CCA GAA ACT GAT TCA GAA GAA GAA GTA  
 Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val  
 235 240 245

20 ACA ATC AAA GCT AAC CTA ATC TTT GCA AAT GGA AGC ACA CAA ACT GCA  
Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala  
250 255 260 265

25 GAA TTC AAA GGA ACA TTT GAA AAA GCA ACA TCA GAA GCT TAT GCG TAT  
 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr  
 270 . 275 280

30 GCA GAT ACT TTG AAG AAA GAC AAT GGA GAA TAT ACT GTA GAT GTT GCA  
 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala  
           285           290           295

GAT AAA GGT TAT ACT TTA AAT ATT AAA TTT GCT GGA  
Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
300 305

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val  
1 5 10 15

50 Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala  
20 25 30

4/16

5                   Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr  
                   35                          40                          45

Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala  
                   50                          55                          60

10                 Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
                   65                          70                          75

## (2) INFORMATION FOR SEQ ID NO: 5:

## (1) SEQUENCE CHARACTERISTICS:

15                 (A) LENGTH: 216 base pairs  
                   (B) TYPE: nucleic acid  
                   (C) STRANDEDNESS: double  
                   (D) TOPOLOGY: linear

20                 (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

25                 (A) NAME/KEY: CDS  
                   (B) LOCATION: 1..216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30                 AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA                  48  
                   Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
                   80                          85                          90

35                 AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA                  96  
                   Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
                   95                          100                          105

40                 ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCA GAT GCA TTA                  144  
                   Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
                   110                          115                          120

45                 AAG AAG GAC AAT GGA GAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT                  192  
                   Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
                   125                          130                          135                          140

ACT TTA AAT ATT AAA TTT GCT GGA  
                   Thr Leu Asn Ile Lys Phe Ala Gly  
                   145

50                 (2) INFORMATION FOR SEQ ID NO: 6:

5/16

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
       1               5                           10                   15

15 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
       20                                   25                           30

20 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
       35                                   40                           45

25 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
       50                                   55                           60

30 Thr Leu Asn Ile Lys Phe Ala Gly  
       65                                   70

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

40 AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA  
   Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
       75                                   80                           85

48

45 AAC TTA ATC TAT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC AAA GGA  
   Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
       90                                   95                           100

96

6/16

|    |  |     |
|----|--|-----|
|    | ACA TTT GAA GAA GCA ACA GCA GAA GCA TAC AGA TAT GCT GAC TTA TTA          | 144 |
| 5  | Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu          |     |
|    | 105                    110                    115                    120 |     |
|    | GCA AAA GAA AAT GGT AAA TAT ACA GTA GAC GTT GCA GAT AAA GGT TAT          | 192 |
|    | Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr          |     |
| 10 | 125                    130                    135                        |     |
|    | ACT TTA AAT ATT AAA TTT GCT GGA  | 216 |
|    | Thr Leu Asn Ile Lys Phe Ala Gly  |     |
|    | 140  |     |
| 15 |  |     |
|    | (2) INFORMATION FOR SEQ ID NO: 8:  |     |
| 20 | (1) SEQUENCE CHARACTERISTICS:  |     |
|    | (A) LENGTH: 72 amino acids   |     |
|    | (B) TYPE: amino acid   |     |
|    | (D) TOPOLOGY: linear   |     |
| 25 | (xi) MOLECULE TYPE: protein  |     |
|    | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:                                 |     |
|    | Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala          |     |
|    | 1                    5                    10                    15       |     |
| 30 | Asn Leu Ile Tyr Ala Asp Gly Lys Thr Glu Thr Ala Glu Phe Lys Gly          |     |
|    | 20                    25                    30                           |     |
|    | Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu          |     |
|    | 35                    40                    45                           |     |
| 35 | Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr          |     |
|    | 50                    55                    60                           |     |
| 40 | Thr Leu Asn Ile Lys Phe Ala Gly  |     |
|    | 65                    70   |     |
|    | (2) INFORMATION FOR SEQ ID NO: 9:  |     |
| 45 | (i) SEQUENCE CHARACTERISTICS:  |     |
|    | (A) LENGTH: 216 base pairs   |     |
|    | (B) TYPE: nucleic acid   |     |
|    | (C) STRANDEDNESS: single   |     |
|    | (D) TOPOLOGY: linear   |     |
| 50 | (xi) MOLECULE TYPE: DNA (genomic)  |     |
|    | (ix) FEATURE:  |     |

7/16

5  
 (A) NAME/KEY: CDS  
 (B) LOCATION:1..216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

|    |   |     |
|----|---|-----|
| 10 | AAA GAA AAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACT ATT AAA GCA<br>Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala<br>75                       80                       85                            | 48  |
| 15 | AAC TTA ATC TAT GCA GAT GGA AAA ACT CAA ACA GCA GAG TTC AAA GGA<br>Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly<br>90                       95                       100                           | 96  |
| 20 | ACA TTT GCA GAA GCA ACA GCA GAA GCA TAC AGA TAC GCT GAC TTA TTA<br>Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu<br>105                     110                       115                       120 | 144 |
| 25 | GCA AAA GAA AAT GGT AAA TAT ACA GCA GAC TTA GAA GAT GGT GGA TAC<br>Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr<br>125                     130                       135                           | 192 |
|    | —   | 216 |

## 30 (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- 35 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

|    |  |  |
|----|--|--|
| 40 | Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala<br>1                       5                       10                       15 |  |
| 45 | Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly<br>20                     25                       30                          |  |
| 50 | Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu<br>35                     40                       45                          |  |
|    | Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr<br>50                     55                       60                          |  |

8/16

Thr Ile Asn Ile Arg Phe Ala Gly  
 65                           70

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAA GAA ACA CCA GAA CCA GAA GAA GTT ACA ATC AAA GCT AAC TTA  
 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu  
 75                       80                       85

48

ATC TTT GCA GAT GGA AGC ACA CAA AAT GCA GAA TTC AAA GGA ACA TTC  
 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe  
 90                       95                       100

96

GCA AAA GCA GTA TCA GAT GCT TAC GCT GCA GAT GCT TTA AAG AAA  
 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys  
 105                      110                      115                      120

144

GAC AAC GGA GAA TAT ACT GTA GAC GTT GCA GAT AAA GGC TTA ACT TTA  
 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu  
 125                      130                      135

192

40

AAT ATT AAA TTC GCT GGT AAA  
 Asn Ile Lys Phe Ala Gly Lys  
 140

213

45

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

9/16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

5 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu  
   1                 5                 10                 15

Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe  
   20                 25                 30

10 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys  
   35                 40                 45

15 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu  
   50                 55                 60

20 Asn Ile Lys Phe Ala Gly Lys  
   65                 70

## (2) INFORMATION FOR SEQ ID NO: 13:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: DNA (genomic)

30

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

40 AAA GAA AAA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC      48  
   Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn  
   75                 80                 85

45 TTA ATC TTT GCA GAT GGA AAG ACA CAA ACA GCA GAA TTC AAA GGA ACA      96  
   Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr  
   90                 95                 100

50 TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA GAC TTA TTA GCA      144  
   Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala  
   105                 110                 115

10/16

|    |  |     |
|----|--|-----|
|    | AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT GGA AAC ACA          | 192 |
| 5  | Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr          |     |
|    | 120                    125                    130                    135 |     |
|    | ATC AAC ATT AAA TTT GCT GGA  | 213 |
|    | Ile Asn Ile Lys Phe Ala Gly  |     |
| 10 | 140  |     |

## (2) INFORMATION FOR SEQ ID NO: 14:

15                    (1) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 71 amino acids  
                       (B) TYPE: amino acid  
                       (D) TOPOLOGY: linear

20                    (ii) MOLECULE TYPE: protein  
                       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

|    |  |  |
|----|--|--|
|    | Lys Glu Lys Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Val Asn    |  |
|    | 1                    5                    10                    15 |  |
| 25 | Leu Ile Phe Ala Asp Gly Lys Thr Gin Thr Ala Glu Phe Lys Gly Thr    |  |
|    | 20                    25                    30                     |  |
|    | Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asp Leu Leu Ala    |  |
| 30 | 35                    40                    45                     |  |
|    | Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly Gly Asn Thr    |  |
|    | 50                    55                    60                     |  |
| 35 | Ile Asn Ile Lys Phe Ala Gly  |  |
|    | 65                    70   |  |

## (2) INFORMATION FOR SEQ ID NO: 15:

40                    (i) SEQUENCE CHARACTERISTICS:  
                       (A) LENGTH: 222 base pairs  
                       (B) TYPE: nucleic acid  
                       (C) STRANDEDNESS: double  
                       (D) TOPOLOGY: linear

45                    (ii) MOLECULE TYPE: DNA (genomic)

50                    (ix) FEATURE:  
                       (A) NAME/KEY: CDS  
                       (B) LOCATION:1..222

11/16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

|    |   |      |
|----|---|------|
| 5  | AAA GAA ACA CCA GAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC<br>Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile<br>75                       80                       85                          | 48   |
| 10 | AAA GTT AAC TTA ATC TTT GCA GAT GGA AAG ATA CAA ACA GCA GAA TTC<br>Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe<br>90                       95                       100                         | 96 — |
| 15 | AAA GGA ACA TTT GAA GAA GCA ACA GCA AAA GCT TAT GCT TAT GCA AAC<br>Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn<br>105                   110                       115                           | 144  |
| 20 | TTA TTA GCA AAA GAA AAT GGC GAA TAT ACA GCA GAC TTA GAA GAT GGT<br>Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly<br>120                   125                       130                       135 | 192  |
| 25 | GGA AAC ACA ATC AAC ATT AAA TTT GCT GGA<br>Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly<br>140                   145   | 222  |

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

|    |  |  |
|----|--|--|
| 30 | Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile<br>1                       5                       10                       15 |  |
| 35 | Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Ile Gln Thr Ala Glu Phe<br>20                   25                       30                            |  |
| 40 | Lys Gly Thr Phe Glu Glu Ala Thr Ala Lys Ala Tyr Ala Tyr Ala Asn<br>35                   40                       45                            |  |
| 45 | Leu Leu Ala Lys Glu Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly<br>50                   55                       60                            |  |
| 50 | Gly Asn Thr Ile Asn Ile Lys Phe Ala Gly<br>65                   70   |  |

## (2) INFORMATION FOR SEQ ID NO: 17:

12/16

5 (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

15 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION.1..225

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAA GAA ACA CCA GAA ACA CCA GAA GAA CCA AAA GAA GAA GTT ACA ATC 48  
Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile  
75 80 85 90

25 AAA GTT AAC TTA ATC TTT GCA GAT GGA AAA ACA CAA ACA GCA GAA TTC 96  
Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe  
95 100 105

30 AAA GGA ACA TTT GAA GAA GCA ACA GCA GAA GCT TAC AGA TAT GCA GAC 144  
Lys Gly Thr Phe Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp  
110 115 120

35 TTA TTA GCA AAA GTA AAT GGT GAA TAC ACA GCA GAC TTA GAA GAT GGC 192  
Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly  
125 130 135

40 (2) INFORMATION FOR SEQ ID NO: 18:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

60 Lys Glu Thr Pro Glu Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile  
1 5 10 15

13/16

Lys Val Asn Leu Ile Phe Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe  
 20 25 30

5

Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp  
 35 40 45

10

Leu Leu Ala Lys Val Asn Gly Glu Tyr Thr Ala Asp Leu Glu Asp Gly  
 50 55 60

Gly Tyr Thr Ile Asn Ile Lys Phe Ala Gly Lys  
 65 70 75

15

(2) INFORMATION FOR SEQ ID NO: 19:

(1) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION.1..246

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA  
 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu  
 1 5 10 15

48

40

CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA  
 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly  
 20 25 30

96

45

AAG ATA CAA ACA GCA GAA CAT AAA GGA ACA TTT GAA GAA GCA ACA GCA  
 Lys Ile Gln Thr Ala Glu His Lys Gly Thr Phe Glu Glu Ala Thr Ala  
 35 40 45

144

50

GAA GCT TAC AGA TAT GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT  
 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr  
 50 55 60

192

55

ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT  
 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala  
 65 70 75 80

240

14/16

5           GGA AAA TAA  
Gly Lys

249

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

10           (A) LENGTH: 249 base pairs  
              (B) TYPE: nucleic acid  
              (C) STRANDEDNESS: double  
              (D) TOPOLOGY: linear

15           (11) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

20           (A) NAME/KEY: CDS  
              (B) LOCATION.1..246

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

25           ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA  
              Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu  
              1               5               10               15

48

30           CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA  
              Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly  
              20               25               30

96

35           AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA  
              Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala  
              35               40               45

144

40           GAA GCT TAC AGA AAC GCA GAC TTA TTA GCA AAA GTA AAT GGC GAA TAT  
              Glu Ala Tyr Arg Phe Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr  
              50               55               60

192

45           ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT  
              Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala  
              65               70               75               80

240

50           GGA AAA TAA  
Gly Lys

249

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

50           (A) LENGTH: 249 base pairs  
              (B) TYPE: nucleic acid  
              (C) STRANDEDNESS: double

15/16

## (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

10 (A) NAME/KEY: CDS  
(B) LOCATION:1..246

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

|    |  |     |
|----|--|-----|
| 15 | ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA<br>Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu | 48  |
|    | 1               5               10               15  |     |
| 20 | CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA<br>Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly | 96  |
|    | 20               25               30   |     |
| 25 | AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA<br>Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala | 144 |
|    | 35               40               45   |     |
| 30 | GAA GCT TAC AGA TAT GCA GAC TTA GAC GCA AAA GTA AAT GGC GAA TGG<br>Glu Ala Tyr Arg Tyr Ala Asp Leu Asp Ala Lys Val Asn Gly Glu Trp | 192 |
|    | 50               55               60   |     |
| 35 | ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT<br>Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala | 240 |
|    | 65               70               75               80  |     |
| 40 | GGA AAA TAA<br>Gly Lys   | 249 |

## (2) INFORMATION FOR SEQ ID NO: 22:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION:1..246

16/16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

|    |   |      |
|----|---|------|
| 5  | ATG AAC ATT AAA TTT GCT GGA AAA GAA ACA CCA GAA ACA CCA GAA GAA<br>Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu<br>1               5               10               15   | 48   |
| 10 | CCA AAA GAA GAA GTT ACA ATC AAA GTT AAC TTA ATC TTT GCA GAT GGA<br>Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly<br>20               25               30                  | 96 — |
| 15 | AAG ATA CAA ACA GCA GAA TTC AAA GGA ACA TTT GAA GAA GCA ACA GCA<br>Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala<br>35               40               45                  | 144  |
| 20 | GAA GCT TAC AGA TAT GCA GAC TTA CAT GCA AAA GTA AAT GGC GAA TAT<br>Glu Ala Tyr Arg Tyr Ala Asp Leu His Ala Lys Val Asn Gly Glu Tyr<br>50               55               60                  | 192  |
| 25 | ACA GCA GAC TTA GAA GAT GGT GGA AAC CAT ATG AAC ATT AAA TTT GCT<br>Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala<br>65               70               75               80 | 240  |
| 30 | GGA AAA TAA<br>Gly Lys  | 249  |
| 35 |   |      |
| 40 |   |      |